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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/873,881	06/04/2001	Fred W. Scott	18617.NEW

CONFIRMATION NO. 6373

FORMALITIES LETTER



OC000000006309437

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Date Mailed: 07/18/2001

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

- For Rules Interpretation, call (703) 308-4216
- To Purchase PatentIn Software, call (703) 306-2600
- For PatentIn Software Program Help, call (703) 306-4119 or e-mail at patin21help@uspto.gov or patin3help@uspto.gov

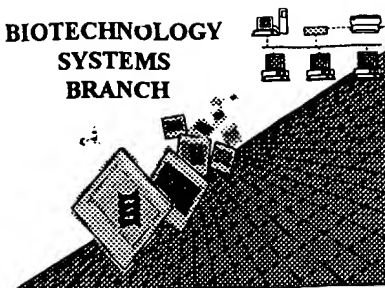
*A copy of this notice **MUST** be returned with the reply.*

Customer Service Center
Initial Patent Examination Division (703) 308-1202

PART 3 - OFFICE COPY

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,881

Source: OPE

Date Processed by STIC: 6/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/873,881

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.

- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001

TIME: 17:28:36

Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Scott, Fred W.
 5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
 7 <130> FILE REFERENCE: 18617.0016
 OK-> 9 <140> CURRENT APPLICATION NUMBER: US/09/873,881
 et-> 11 <141> CURRENT FILING DATE: 2001-06-04
 13 <160> NUMBER OF SEQ ID NOS: 25

ERRORED SEQUENCES

212 <210> SEQ ID NO: 2
 214 <211> LENGTH: 1575
 216 <212> TYPE: DNA
 218 <213> ORGANISM: rabies virus
 220 <220> FEATURE:
 222 <223> OTHER INFORMATION:
 E--> 224 <400> SEQUENCE: *2 ← insert sequence number*
 225 atg gtt cct cag gct ctc ctg ttt gta ccc ctt ctg gtt ttt 42
 226 Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe
 W--> 227 1 5 10
 229 cca ttg tgt ttt ggg aaa ttc cct att tac acg ata cta gac 84
 230 Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp
 W--> 231 15 20 25
 233 aag ctt ggt ccc tgg agc ccg att gac ata cat cac ctc agc 126
 234 Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser
 W--> 235 30 35 40
 237 tgc cca aac aat ttg gta gtg gag gac gaa gga tgc acc aac 168
 238 Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn
 W--> 239 45 50 5
 241 ctg tca ggg ttc tcc tac atg gaa ctt aaa gtt gga tac atc 210
 242 Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile
 W--> 243 60 65
 245 tta gcc ata aaa atg aac ggg ttc act tgc aca ggc gtt gtg 252
 246 Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val
 W--> 247 75 80
 249 acg gag gct gaa acc tac act aac ttc gtt ggt tat gtc aca 294
 250 Thr Glu Ala Glu Thr Tyr Asn Phe Val Gly Tyr Val Thr
 W--> 251 85 90 95
 253 acc acg ttc aaa aga aag cat ttc cgc cca aca cca gat gca 336
 254 Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
 W--> 255 100 105 110
 257 tgt aga gcc gcg tac aac tgg aag atg gcc ggt gac ccc aga 378
 258 Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg
 W--> 259 115 120 125
 261 tat gaa gag tct cta cac aat ccg tac cct gac tac cgc tgg 420

*This error also
 exists in figure 1*
 ↓
*misaligned
 amino acid
 numbers -
 see item 3 on
 Error Summary
 sheet*

262 Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp
W--> 263 130 135 140

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

	265	ctt	cga	act	gta	aaa	acc	acc	aag	gag	tct	ctc	gtt	atc	ata	462
	266	Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile	
W-->	267					145				150						
	269	tct	cca	agt	gta	gca	gat	ttg	gac	cca	tat	gac	aga	tcc	ctt	504
	270	Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu	
W-->	271	155				160				165						
	273	cac	tcg	agg	gtc	ttc	cct	agc	ggg	aag	tgc	tca	gga	gta	gcg	546
	274	His	Ser	Arg	Val	Phe	Pro	Ser	Gly	Lys	Cys	Ser	Gly	Val	Ala	
W-->	275	170				175				180						
	277	gtg	tct	tct	acc	tac	tgc	tcc	act	aac	cac	gat	tac	acc	att	588
	278	Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile	
W-->	279					185				190				195		
	281	tgg	atg	ccc	gag	aat	ccg	aga	cta	ggg	atg	tct	tgt	gac	att	630
	282	Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile	
W-->	283					200				205				210		
	285	ttt	acc	aat	agt	aga	ggg	aag	aga	gca	tcc	aaa	ggg	agt	gag	672
	286	Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu	
W-->	287					215				220						
	289	act	tgc	ggc	ttt	gta	gat	gaa	aga	ggc	cta	tat	aag	tct	tta	714
	290	Thr	Cys	Gly	Phe	Val	Asp	Glu	Arg	Gly	Leu	Tyr	Lys	Ser	Leu	
W-->	291	225				230				235						
	293	aaa	gga	gca	tgc	aaa	ctc	aag	tta	tgt	gga	gtt	cta	gga	ctt	756
	294	Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu	
W-->	295	240				245				250						
	297	aga	ctt	atg	gat	gga	aca	tgg	gtc	gcg	atg	caa	aca	tca	aat	798
	298	Arg	Leu	Met	Asp	Gly	Thr	Trp	Val	Ala	Met	Gln	Thr	Ser	Asn	
W-->	299					255				260				265		
	301	gaa	acc	aaa	tgg	tgc	gct	ccc	gat	cag	ttg	gtg	aac	ctg	cac	840
	302	Glu	Thr	Lys	Trp	Cys	Pro	Pro	Asp	Gln	Leu	Val	Asn	Leu	His	
W-->	303					270				275				280		
	305	gac	ttt	cgc	tca	gac	gaa	att	gag	cac	ctt	gtt	gta	gag	gag	882
	306	Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu	
W-->	307					285				290						
	309	ttg	gtc	agg	aag	aga	gag	gag	tgt	ctg	gat	gca	cta	gag	tcc	924
W-->	310	Leu	Val	Arg	Lys	Arg	Glu	Glu	Cys	Leu	Asp	Ala	Leu	Glu	Ser	
W-->	311	295				300				305						
	313	atc	atg	aca	aac	aag	tca	gtg	agt	ttc	aga	cgt	ctc	agt	cat	966
	314	Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His	
W-->	315	310				315				320						
	317	tta	aga	aaa	ctt	gtc	cct	ggg	ttt	gga	aaa	gca	tat	acc	ata	1008
	318	Leu	Arg	Lys	Leu	Val	Pro	Gly	Phe	Gly	Lys	Ala	Tyr	Thr	Ile	
W-->	319					325				330				335		
	321	ttc	aac	aag	acc	ttg	atg	gaa	gcc	gat	gct	cac	tac	aag	tca	1050
	322	Phe	Asn	Lys	Thr	Leu	Met	Glu	Ala	Asp	Ala	His	Tyr	Lys	Ser	
W-->	323															
										340						345
	325	gtc	aga	act	tgg	aat	gag	atc	ctc	cct	tca	aaa	ggg	tgt	tta	1092
	326	Val	Arg	Thr	Trp	Asn	Glu	Ile	Leu	Pro	Ser	Lys	Gly	Cys	Leu	
W-->	327													355		360
	329	aga	gtt	ggg	ggg	agg	tgt	cat	cct	cat	gtg	aac	ggg	gtg	ttt	1134

misaligned
amino
acid
nos.

RAW SEQUENCE LISTING

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DATE: 06/21/2001

TIME: 17:28:36

Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

misaligned nos.

```

330 Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe
W--> 331                                     365                 370
333 ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc
334 Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile
W--> 335
                                     380                 385                 390
337 cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg
338 Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu
W--> 339
                                     395                 400                 40
341 ttg gaa tcc tcg gtt atc ccc ctt gtg cac ccc ctg gca gac
342 Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp
W--> 343
                                     410                 415
346 ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt
347 Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe
W--> 348
                                     425                 430
350 gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga
351 Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly
W--> 352
                                     435                 440                 445
354 gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg
355 Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu
W--> 356
                                     450                 455                 460
358 agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg
359 Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu
W--> 360
                                     465                 470                 47
362 atg aca tgt tgt aga aga gtc aat cga tca gaa cct acg caa
363 Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln
W--> 364
                                     480                 485
366 cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc
367 His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro
W--> 368
                                     495                 500                 505
370 caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt
371 Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser
W--> 372
                                     505                 510                 515
374 ggg ggt gag acc aga ctg tga 1575
375 Gly Gly Glu Thr Arg Leu
W--> 376
                                     520
379 <210> SEQ ID NO: 3
381 <211> LENGTH: (44) 40 shown
383 <212> TYPE: DNA
385 <213> ORGANISM: P11 late promoter and leader sequence
387 <220> FEATURE:
389 <223> OTHER INFORMATION:
E--> 391 <400> SEQUENCE: 3 ←
E--> 392 taaaaatata gtagaatttc attttgtttt tttctatgct
394 <210> SEQ ID NO: 4
396 <211> LENGTH: 28
398 <212> TYPE: DNA
400 <213> ORGANISM: artificial sequence

```

524 number the amino acids under every 5 amino acids

40 ← insert cumulative base noted at right margin of each line

402 <220> FEATURE:

404 <223> OTHER INFORMATION: forward primer

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

E--> 406 <400> SEQUENCE: 4<

407 cgggatccat ttttccttcg ttgccat 28

410 <210> SEQ ID NO: 5

412 <211> LENGTH: 28

414 <212> TYPE: DNA

416 <213> ORGANISM: artificial sequence

W--> 418 <220> FEATURE: reverse primer

420 <223> OTHER INFORMATION:

E--> 422 <400> SEQUENCE: 5<

423 cgggtaccga tttctccgtg ataggtat 28

426 <210> SEQ ID NO: 6

428 <211> LENGTH: 18

430 <212> TYPE: DNA

432 <213> ORGANISM: artificial sequence

W--> 434 <220> FEATURE: sequencing primer

436 <223> OTHER INFORMATION:

E--> 438 <400> SEQUENCE: 6<

439 ctacttgcac agataggt 18

443 <210> SEQ ID NO: 7

445 <211> LENGTH: 2007

447 <212> TYPE: DNA

449 <213> ORGANISM: feline calicivirus

451 <220> FEATURE:

453 <223> OTHER INFORMATION:

E--> 455 <400> SEQUENCE: ① 7<

456 atg tgc tca acc tgc gct aac gtg ctt aaa tac tat gat tgg gat 45

457 Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp

W--> 458

460 cct cac atc aaa ttg gta atc aac ccc aac aaa ttt cta cat gtt 90

461 Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val

W--> 462

464 ggc ttc tgc gat aac cct tta atg tgt tgt tat cct gaa tta cta 135

465 Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu

W--> 466

468 cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa 180

469 Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln

W--> 470

472 gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act 225

473 Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr

W--> 474

476 cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa 270

477 His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu

W--> 478

480 gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac 315

481 Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His

W--> 482

move down to C2237 line - do not insert any
response to C2207;
C2207 is a header
only

misaligned
amino acid
nos.

1 5 10

90

20 25

135

35 40

180

50 55

225

65 70

270

80 85

315

95 100

484 ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt 360
485 Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu

W--> 486

110

115

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

*misaligned
amino acid
pos.*

488	ttc cgc ttg gaa gcg gac gat ggt tcc atc acg aca cct gaa cag	405	
489	Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln		
W--> 490			
		125	130
492	gga aca atg gtt ggt gga gtc att gct gag ccc aac gcc caa atg	450	
493	Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met		
W--> 494			
		140	145
496	tca acc gca gct gac atg gcc act ggg aaa agt gtg gac tct gag	495	
497	Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu		
W--> 498			
		155	160
500	tgg gaa gcc ttc ttc tcc ttt cac act agt gtg aac tgg agc aca	540	
501	Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val Asn Trp Ser Thr		
W--> 502			
		170	175
504	tct gaa act cag ggg aag ata ctc ttt aaa caa tcc tta gga cca	585	
505	Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser Leu Gly Pro		
W--> 506			
		185	190
508	ttg ctc aac ccc tac ctt acc cat ctt gca aag ctg tat gtt gct	630	
509	Leu Leu Asn Pro Tyr Leu Thr His Leu Ala Lys Leu Tyr Val Ala		
W--> 510			
		200	205
512	tgg tct ggt tct gtt gat gtt agg ttt tct att tct gga tct ggt	675	
513	Trp Ser Gly Ser Val Asp Val Arg Phe Ser Ile Ser Gly Ser Gly		
W--> 514			
		215	220
516	gtc ttt gga ggg aaa tta gct gct att gtt gtg ccg cca gga att	720	
517	Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Ile		
W--> 518			
		230	235
520	gat cct gtt caa agt act tca atg ctg caa tat cct cat gtc ctc	765	
521	Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu		
W--> 522			
		245	250
524	ttt gat gct cgt caa gtt gaa cct gtt atc ttt tcc att ccc gat	810	
525	Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Ser Ile Pro Asp		
W--> 526			
		260	265
528	cta aga agc acc tta tat cac ctt atg tct gac act gat acc aca	855	
529	Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr		
W--> 530			
		275	280
532	tcg ttg gta atc atg gtg tac aat gat ctt att aac ccc tat gct	900	
533	Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala		
W--> 534			
		290	295
536	aat gac tca aac tct tcg ggc tgc att gtc act gtg gaa act aaa	945	
537	Asn Asp Ser Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys		
W--> 538			
		305	310
540	ccg ggg cca gat ttc aag ttt cac ctc tta aaa cct cct ggg tct	990	

541	Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser		
W--> 542		320	325
544	atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca	1035	
545	Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser		
W--> 546		335	340
548	tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080	345
549	Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp		
W--> 550		350	355
552	ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat	1125	360

misaligned nos.

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing - Scott et al

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*misaligned
arrow and nos.*

553 Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp		
W--> 554	365	370 375
556 ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca		1170
557 Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro		
W--> 558	380	385 390
560 att act atc act atc agt gtt aag gag tca gca aag ctt ggt att		1215
561 Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile		
W--> 562	395	400 405
564 gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg		1260
565 Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp		
W--> 566	410	415 420
568 ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat		1305
569 Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr		
W--> 570	425	430 435
572 gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag		1350
573 Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln		
W--> 574	440	445 450
576 tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc		1395
577 Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly		
W--> 578	455	460 465
580 atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag		1440
581 Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys		
W--> 582	470	475 480
584 att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc		1485
585 Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala		
W--> 586	485	490 495
588 aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta		1530
589 Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val		
W--> 590	500	505 510
592 ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac		1575
593 Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp		
W--> 594	515	520 525
596 aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att		1620
597 Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile		
W--> 598	530	535 540
600 ggt gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa		1665
601 Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu		
W--> 602	545	550 555
604 cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct		1710
605 Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser		
W--> 606		

misaligned 1081

	560	565	570
608 atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct		1755	
609 Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser			
W--> 610			
	575	580	585
612 caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta		1800	
613 Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu			
W--> 614			
	590	595	600
616 ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat		1845	
617 Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn			

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*misaligned
nos.*

W--> 618

620 gga tcc tgg ttt gac ata ggc att gat aat gat gga ttt tct ttt 1890

621 Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe

W--> 622

624 gtt ggt gta tca agt att ggt aaa tta gag ttt cct tta act gcc 1935

625 Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala

W--> 626

628 tcc tac atg gga att caa ttg gca aaa att cga ctt gcc tct aac 1980

629 Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn

W--> 630

632

633 Ile Arg Ser Val Met Thr Lys Leu


W--> 634

665

637 <210> SEQ ID NO: 8

639 <211> LENGTH: 582

641 <212> TYPE: DNA

643 <213> ORGANISM: artificial sequenceW--> 645 <220> FEATURE: hemagglutinin left arm647 <223> OTHER INFORMATION: 

E--> 649 <400> SEQUENCE: ①8<

650 attaaacgca aatatccatg gaaaacgcgc agtatacaga cgatttttta 50

651 cagtatttgg agagttttat aggaagtata tagagtagaa ccagaatttt 100

652 gtaaaaaata atcacatttt tatactaata tgaaacaact atcgatagtt 150

653 atattgctac tatcgatagt atatacaacc aaacctcatc ctacacagat 200

654 atcaaaaaaa ctaggcgatg atgtactct atcgtgtaat agaaacaata 250

655 cacatggata tcttgcacatg agttcttggg ataagaaacc agactccatt 300

656 attctcttag cagccaaaaa cgaatgcgta tactttgatg attatacagc 350

657 ggataaagta tcatacgatt caccgtatga tactctagct acaattatta 400

658 caattaaatc attgacatct gcagatgcag gtacttatat atgcgcattc 450

659 tttataacat caacaaatga tacggataaa atagattatg aagaatactt 500


660 catagatttg gttgtaaatc cagctaattg atccactatt gacgcgattc 550

661 tatcaggatc taatttctcc gtgataggta tc 582

662 <210> SEQ ID NO: 9

664 <211> LENGTH: 447

666 <212> TYPE: DNA

668 <213> ORGANISM: artificial sequenceW--> 670 <220> FEATURE: hemagglutinin right arm672 <223> OTHER INFORMATION: 

E--> 674 <400> SEQUENCE: ①9<

675 ctctagcgcc taaccccagg cgaccgacga caacctttat gatacatata 50

676 atgaaccaat atctgtatca tcctcgatac caacaacggt agaaagtgtt 100

677 acaatatcta ctacaaaata tacaactagt gactttatag agatatttgg 150

678 cattgtttca ctaattttat tattggccgt ggcgatttcc tgtattatat 200

679 tatttctgta gtggacggtc tcgtaaacaa gaaacaaata tattatagat 250

680 ttttaactcag ataaatgtct ggaataatta aatctatcgt tttgagcgga 300

681 ccatctggtt ccggcaagac agctatagtc aggagactct tacaagatta 350

682 tggaaatata tttggatttg tggatccca taccactaga tttcctcgtc 400

683 ctatggaacg agaaggtgtc gactaccatt acgttaacag agaggcc 447

686 <210> SEQ ID NO: 10

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Output Set: N:\CRF3\06212001\I873881.raw

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688 <211> LENGTH: 40
690 <212> TYPE: DNA
692 <213> ORGANISM: artificial sequence
W--> 694 <220> FEATURE: primer P3
696 <223> OTHER INFORMATION:
E--> 698 <400> SEQUENCE: ① 106
699 gatacctatc acggagaaat tagatcctga tagaatcgcg 40
702 <210> SEQ ID NO: 11
704 <211> LENGTH: 22
706 <212> TYPE: DNA
708 <213> ORGANISM: artificial sequence
W--> 710 <220> FEATURE: primer P1
712 <223> OTHER INFORMATION:
E--> 714 <400> SEQUENCE: ① 11
715 attaaacgca aatatccatg gg 22
718 <210> SEQ ID NO: 12
720 <211> LENGTH: 27
722 <212> TYPE: DNA
724 <213> ORGANISM: artificial sequence
W--> 726 <220> FEATURE: primer F2
728 <223> OTHER INFORMATION:
E--> 730 <400> SEQUENCE: ① 12
731 gcggtaccct ggggttaggc gatagag 27
734 <210> SEQ ID NO: 13
736 <211> LENGTH: 20
738 <212> TYPE: DNA
740 <213> ORGANISM: artificial sequence
W--> 742 <220> FEATURE: primer P5
744 <223> OTHER INFORMATION:
E--> 746 <400> SEQUENCE: ① 136
747 atttctccgt gataggtatc 20
750 <210> SEQ ID NO: 14
752 <211> LENGTH: 22
754 <212> TYPE: DNA
756 <213> ORGANISM: artificial sequence
W--> 758 <220> FEATURE: primer P5
760 <223> OTHER INFORMATION:
E--> 762 <400> SEQUENCE: ① 146
763 ggcctctctg ttaacgtaat gg 22
766 <210> SEQ ID NO: 15
768 <211> LENGTH: 22
770 <212> TYPE: DNA
772 <213> ORGANISM: artificial sequence
W--> 774 <220> FEATURE: primer P2
776 <223> OTHER INFORMATION:
E--> 778 <400> SEQUENCE: ① 15
779 gcgtcgaagt ttgagcatgt gc 22
782 <210> SEQ ID NO: 16
784 <211> LENGTH: 40

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Input Set : A:\Sequence Listing - Scott et al

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786 <212> TYPE: DNA
788 <213> ORGANISM: artificial sequence
W--> 790 <220> FEATURE: primer P4
792 <223> OTHER INFORMATION:
E--> 794 <400> SEQUENCE: ①/6
795 ctctagcgcc taaccccagg cgaccgacga caacctttat 40
799 <210> SEQ ID NO: 17
801 <211> LENGTH: 840
803 <212> TYPE: DNA
805 <213> ORGANISM: feline infectious peritonitis virus
807 <220> FEATURE:
809 <223> OTHER INFORMATION:
E--> 811 <400> SEQUENCE: ①/76
812 aaaccaaggc atataatccc gacgaagcat ttttggttg aactaaacaa a 51
814 atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96
815 Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
W--> 816
818 tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141
819 Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
W--> 820
822 att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186
823 Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
W--> 824
826 gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231
827 Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
W--> 828
830 ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276
831 Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
W--> 832
834 ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta 321
835 Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu
W--> 836
838 tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct 366
839 Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser
W--> 840
842 gag tac caa gtt tcc aga tat gta atg ttc ggc ttt agt gtt gca 411
843 Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala
W--> 844
846 ggt gca gtt gta acg ttt gca ctt tgg atg atg tat ttt gtg aga 456
847 Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg
W--> 848
850 tct gtt cag cta tat aga aga acc aaa tca tgg tgg tct ttt aat 501
W--> 851 Ser Val Gln Leu Tyr Arg Axa Thr Lys Ser Trp Trp Ser Phe Asn
W--> 852

*misaligned
amino acid
nos.*

1 5 10
20 25
35 40
50 55
65 70
80 85
95 100
110 115
125 130

		140	145
854	cct gag act aat gca att ctt tgt gtt aat gca ttg ggt aga agt	546	
855	Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser		
W--> 856			
		155	160
858	tat gtg ctt ccc tta gat ggt act cct aca ggt gtt acc ctt act	591	
859	Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr		

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Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

*mesalysed amino
hos*

W--> 860

862 cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt
 863 Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly

170
636

175

W--> 864

866 ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca
 867 Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr

185
681

190

W--> 868

870 cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa
 871 Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys

200
726

205

W--> 872

874 gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct
 875 Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala

215
771

220

W--> 876

878 ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat
 879 Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His

230
816

235

W--> 880

882 gaa aaa tta tta cat atg gtg taa 840
 883 Glu Lys Leu Leu His Met Val
 884 260

245

250

886 <210> SEQ ID NO: 18

888 <211> LENGTH: 1144

890 <212> TYPE: DNA

892 <213> ORGANISM: feline infectious peritonitis virus

894 <220> FEATURE:

896 <223> OTHER INFORMATION:

E--> 898 <400> SEQUENCE: ①186

899 atg gcc aca cag gga caa cgc gtc aac tgg gga gat gaa cct tcc
 900 Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser

45

W--> 901

903 aaa aga cgt ggt cgt tct aac tct cgt ggt cgg aag aat aat gat
 904 Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp

5 10

90

W--> 905

907 ata cct ttg tca ttc tac aac ccc att acc ctc gaa caa gga tct
 908 Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser

20 25

135

W--> 909

911 aaa ttt tgg aat tta tgt ccg aga gac ctt gtt ccc aaa gga ata
 912 Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile

35 40

180

W--> 913

915 ggt aat aag gat caa caa att ggt tat tgg aat aga cag att cgt
 916 Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg

50 55

225

W--> 917

919 tat cgt att gta aaa ggc cag cgt aag gaa ctc gct gag agg tgg

65 70

270

*mesalysed
amino acid
hos*

misaligned has.

920 Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp
W--> 921
923 ttc ttt tac ttc tta ggt aca gga cct cat gct gat gct aaa ttc
924 Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
W--> 925
927 aaa gac aag att gat gga gtc ttc tgg gtt gca agg gat ggt gcc
928 Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala

80

85

315

95

100

360

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Input Set : A:\Sequence Listing - Scott et al

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*misaligned
ho3.*

W--> 929		110	115
931 atg aac aag ccc aca acg ctt ggc act cgt gga acc aat aac gaa	405		
932 Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu			
W--> 933		125	130
935 tcc aaa cca ctg aga ttt gat ggt aag ata ccg cca cag ttt cag	450		
936 Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln			
W--> 937		140	145
939 ctt gaa gtg aac cgt tct agg aac aat tca agg tct ggt tct cag	495		
940 Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln			
W--> 941		155	160
943 tct aga tct gtt tca aga aac aga tct caa tct aga gga aga cac	540		
944 Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His			
W--> 945		170	175
947 cat tcc aat aac cag aat aat aat gtt gag gat aca att gta gcc	585		
948 His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala			
W--> 949		185	190
951 gtg ctt gaa aaa tta ggt gtt act gac aaa caa agg tca cgt tct	630		
952 Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser			
W--> 953		200	205
955 aaa cct aga gaa cgt agt gat tcc aaa cct agg gac aca aca cct	675		
956 Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro			
W--> 957		215	220
959 aag aat gcc aac aaa cac acc tgg aag aaa act gca ggc aag gga	720		
960 Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly			
W--> 961		230	235
963 gat gtg aca act ttc tat ggt gct aga agt agt tca gct aac ttt	765		
964 Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe			
W--> 965		245	250
967 ggt gat agt gat ctc gtt gcc aat ggt aac gct gcc aaa tgc tac	810		
968 Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr			
W--> 969		260	265
971 cct cag ata gct gaa tgt gtt cca tca gtg tct agc ata atc ttt	855		
972 Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe			
W--> 973		275	280
975 ggc agt caa tgg tct gct gaa gaa gct ggt gat caa gtg aaa gtc	900		
976 Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val			
W--> 977		290	295
979 acg ctc act cac acc tac tac ctg cca aag gat gat gcc aaa act	945		
980 Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr			
W--> 981			

misaligned

	983 agt caa ttc cta gaa cag att gac gct tac aag cga cct tct gaa	305	310
W-->	984 Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu	990	
W-->	985		
	987 gtg gct aag gat cag agg caa aga aga tcc cgt tct aag tct gct	320	325
	988 Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala	1035	
W-->	989		
		335	345
	991 gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac	340	
	992 Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr	1080	
W-->	993		
		350	360
		355	

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995 aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt 1125
 996 Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
 W--> 997

999 acg aac taa acgcatgctc 1144
 1000 Thr Asn
 1001 377
 1004 <210> SEQ ID NO: 19
 1006 <211> LENGTH: (1979) 1980
 1008 <212> TYPE: DNA
 1010 <213> ORGANISM: feline leukemia virus
 1012 <220> FEATURE:
 1014 <223> OTHER INFORMATION:

E--> 1016 <400> SEQUENCE: (1) 195
 E--> 1017 accaccaatc aagacctctc ggaagagccc agctcagacg atccatcaag
 E--> 1019 atg gaa agt cca acg cac cca aaa ccc tct aaa gat aag act ctg
 1020 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
 W--> 1021

E--> 1023 tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac
 1024 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
 W--> 1025

E--> 1027 ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act
 1028 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
 W--> 1029

E--> 1031 tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc
 1032 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr
 1033 50 55 60
 E--> 1035 tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt 275
 1036 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val
 1037 65 70 75
 E--> 1039 gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta 320
 1040 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu
 1041 80 85 90
 E--> 1043 aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa 365
 1044 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys
 W--> 1045 95 100 105
 E--> 1047 tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac 410
 1048 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr
 W--> 1049 110 115 120
 E--> 1051 ccc ttt tac gtc tgc ccc gga cat gcc ccc tcg ttg ggg cca aag 455
 1052 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys
 W--> 1053 125 130 135
 E--> 1055 gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg 500
 1056 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
 W--> 1057 140 145 150
 E--> 1059 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca 545
 1060 Gly Cys Glu Thr Thr Gly Glu Thr Trp Lys Pro Thr Ser Ser
 W--> 1061 155 160 165
 E--> 1063 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc 590
 1064 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser

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W--> 1065	170	175	180	
E--> 1067 tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag				635
1068 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys				
W--> 1069	185	190	195	
E--> 1072 gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga				680
1073 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg				
W--> 1074	200	205	210	
E--> 1076 cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc				725
1077 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser				
W--> 1078				
			215	220
E--> 1080 cgg cag gta tca acc att acg ccg cct cag gca atg gga cca aac				770
1081 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn				
W--> 1082	230	235	240	
E--> 1084 cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca				815
1085 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr				
W--> 1086	245	250	255	
E--> 1088 ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc				860
1089 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala				
W--> 1090	260	265	270	
E--> 1092 cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg				905
1093 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly				
W--> 1094	275	280	285	
E--> 1096 acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc				950
1097 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala				
W--> 1098	290	295	300	
E--> 1100 tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc				995
1101 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys				
W--> 1102	305	310	315	
E--> 1104 ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt				1040
1105 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly				
W--> 1106	320	325	330	
E--> 1108 acc tac agc aac caa aca aac ccc ccc cca tcc tgc cta tct act				1085
1109 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile				
W--> 1110	335	340	345	
E--> 1114 ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg				1130
1115 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met				
W--> 1116	350	355	360	
E--> 1118 tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag				1175
1119 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys				
W--> 1120	365	370	375	
E--> 1122 aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac				1220
1123 Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn				
W--> 1124	380	385	390	
E--> 1126 ggc acc tat tgg gcc tgt aac act gga ctc acc cca tgc att tcc				1265
1127 Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser				
W--> 1128	395	400	405	
E--> 1130 atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa				1310
1131 Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu				
W--> 1132	410	415	420	

*misaligned
amino
res.*

RAW SEQUENCE LISTING

DATE: 06/21/2001

PATENT APPLICATION: US/09/873,881

TIME: 17:28:37

Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

```

E--> 1134 tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca 1355
      1135 Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
W--> 1136                425                430                435
E--> 1138 cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta 1400
W--> 1139 His Phe Ala Lys Ala Val Arg Phe Arg Axa Glu Pro Ile Ser Leu
W--> 1140                440                445                450
E--> 1142 acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc 1445
      1143 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
W--> 1144                455                460                465
E--> 1146 gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag 1490
      1147 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
W--> 1148                470                475                480
E--> 1151 ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta 1535
      1152 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
W--> 1153                485                490                495
E--> 1156 gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct 1580
      1157 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
W--> 1158                500                505                510
E--> 1160 gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta 1625
      1161 Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu
W--> 1162                515                520                525
E--> 1164 caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc 1670
      1165 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
W--> 1166                530                535                540
E--> 1168 tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta 1715
      1169 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
W--> 1170                545                550                555
E--> 1172 aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag 1760
      1173 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
W--> 1174                560                565                570
E--> 1176 gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc 1805
      1177 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
W--> 1178                575                580                585
E--> 1180 cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att 1850
      1181 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile
W--> 1182                590                595                600
E--> 1184 ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta
W--> 1185 1895 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe
W--> 1186 Val
W--> 1187                605                610                615
E--> 1189 aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag
W--> 1190 1940 Lys Asp Axa Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln
W--> 1191 Gln
W--> 1192                620                625                630
E--> 1194 tac caa cag ata aag caa tac gat ccg gac cga cca tga 1979
      1195 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
E--> 1196                635                640
1199 <210> SEQ ID NO: 20
1201 <211> LENGTH: 584

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```

1280 Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe
E--> 1281          335          340          345
1283 Glu Ala Ser Thr Gln Gly Pro Phe Lys Ile Pro Ile Ala Ala Gly
E--> 1284          350          355          360
1286 Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp
E--> 1287          365          370          375
1289 Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr
E--> 1290          380          385          390
1292 Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp
E--> 1293          395          400          405
1295 Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn Ile Asn Phe
E--> 1296          410          415          420
1298 Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro
E--> 1299          425          430          435
1302 Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr
E--> 1303          440          445          450
1305 Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro
E--> 1306          455          460          465
1309 Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
E--> 1310          470          475          480
1312 Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro
E--> 1313          485          490          495
1315 Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr
E--> 1316          500          505
1319 Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser
E--> 1320          515          520          525
1322 Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg
E--> 1323          530          535          540
1325 Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val
E--> 1326          545          550          555
1328 Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys
E--> 1329          560          565          570
1332 Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg, Lys Leu Tyr
E--> 1333          575
1336 <210> SEQ ID NO: 21
1338 <211> LENGTH: 524
1340 <212> TYPE: PRT
1342 <213> ORGANISM: rabies virus
1344 <220> FEATURE:
1346 <223> OTHER INFORMATION:
E--> 1348 <400> SEQUENCE: ① 21
1349 Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe
E--> 1350          1          5
1352 Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp
E--> 1353          15          20          25
1355 Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser
E--> 1356          30          35          40
1358 Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn
E--> 1359          45          50          5

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*Misaligned
and
nos.*

Misaligned nos.

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Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

```

1362 Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile
E--> 1363
60
1365 Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val
E--> 1366 75
1368 Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr
E--> 1369 85 90 95
1371 Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
E--> 1372 100 105 110
1374 Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg
E--> 1375 115 120 125
1377 Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp
E--> 1378 130 135 140
1380 Leu Arg Thr Val Lys Thr Thr Lys Glu Ser Leu Val Ile Ile
E--> 1381 145 150
1383 Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu
E--> 1384 155 160 165
1386 His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala
E--> 1387 170 175 180
1389 Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile
E--> 1390 185 190 195
1392 Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile
E--> 1393 200 205 210
1395 Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu
E--> 1396 215 220
1398 Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu
E--> 1399 225 230 235
1401 Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu
E--> 1402 240 245 250
1404 Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn
E--> 1405 255 260 265
1407 Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His
E--> 1408 270 275 280
1411 Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu
E--> 1412 285 290
1414 Leu Val Arg Lys Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser
E--> 1415 295 300 305
1417 Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His
E--> 1418 310 315 320
1420 Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
E--> 1421 325 330 335
1423 Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser
E--> 1424
340
1426 Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu
E--> 1427 355
1429 Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe
E--> 1430 365 370
1432 Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile
E--> 1433
380 385
1435 Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu

```

65

80

*misaligned amino
nos.*

345

360

375

390

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Input Set : A:\Sequence Listing - Scott et al

Output Set: N:\CRF3\06212001\I873881.raw

*misaligned
208.*

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E--> 1436                                395      400      40
      1438 Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp
E--> 1439                                410      415
      1441 Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe
E--> 1442                                425      430
      1444 Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly
E--> 1445                                435      440      445
      1447 Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu
E--> 1448                                450      455      460
      1450 Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu
E--> 1451                                465      470      47
      1453 Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln
E--> 1454                                480      485
      1456 His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro
E--> 1457                                495      500
      1459 Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser
E--> 1460                                505      510      515
      1463 Gly Gly Glu Thr Arg Leu
E--> 1464                                520      524
      1467 <210> SEQ ID NO: 22
      1469 <211> LENGTH: 668
      1471 <212> TYPE: PRT
      1473 <213> ORGANISM: feline calicivirus
      1475 <220> FEATURE:
      1477 <223> OTHER INFORMATION:
E--> 1479 <400> SEQUENCE: ① 22 ←
      1480 Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp
E--> 1481                                1      5      10
      1483 Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val
E--> 1484                                20      25
      1486 Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu
E--> 1487                                35      40
      1489 Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln
E--> 1490                                50      55
      1492 Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr
E--> 1493                                65      70
      1495 His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu
E--> 1496                                80      85
      1498 Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His
E--> 1499                                95      100
      1501 Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu

```

E--> 1502

1504 Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln

E--> 1505

1507 Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met

E--> 1508

1510 Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu

E--> 1511

1513 Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val Asn Trp Ser Thr

misaligned 108.

110

115

125

130

140

145

155

160

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
 Output Set: N:\CRF3\06212001\I873881.raw

*misaligned
 h08.*

E--> 1514	170	175
1516 Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser Leu Gly Pro		
E--> 1517	185	190
1519 Leu Leu Asn Pro Tyr Leu Thr His Leu Ala Lys Leu Tyr Val Ala		
E--> 1520	200	205
1522 Trp Ser Gly Ser Val Asp Val Arg Phe Ser Ile Ser Gly Ser Gly		
E--> 1523	215	220
1525 Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Ile		
E--> 1526	230	235
1528 Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu		
E--> 1529	245	250
1531 Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Ser Ile Pro Asp		
E--> 1532	260	265
1534 Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr		
E--> 1535	275	280
1537 Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala		
E--> 1538	290	295
1540 Asn Asp Ser Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys		
E--> 1541	305	310
1543 Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser		
E--> 1544	320	325
1546 Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser		
E--> 1547	335	340
1549 Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp		
E--> 1550	350	355
1552 Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp		
E--> 1553	365	370
1555 Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro		
E--> 1556	380	385
1558 Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile		
E--> 1559	395	400
1561 Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp		
E--> 1562	410	415
1564 Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr		
E--> 1565	425	430
		435

*missed
nos.*

1567 Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln			
E--> 1568	440	445	450
1570 Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly			
E--> 1571	455	460	465
1573 Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys			
E--> 1574	470	475	480
1576 Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala			
E--> 1577	485	490	495
1579 Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val			
E--> 1580	500	505	510
1582 Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp			
E--> 1583	515	520	525
1585 Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile			
E--> 1586	530	535	540

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Input Set : A:\Sequence Listing - Scott et al
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1588 Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu
E--> 1589 545 550 555

1591 Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser
E--> 1592 560 565 570

1594 Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser
E--> 1595 575 580 585

1597 Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu
E--> 1598 590 595 600

1600 Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn
E--> 1601 605 610 615

1603 Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe
E--> 1604 620 625 630

1606 Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala
E--> 1607 635 640 645

1609 Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn
E--> 1610 650 655 660

1612 Ile Arg Ser Val Met Thr Lys Leu
E--> 1613 665

1616 <210> SEQ ID NO: 23
1618 <211> LENGTH: 262
1620 <212> TYPE: PRT
1622 <213> ORGANISM: feline infectious peritonitis virus
1624 <220> FEATURE:
1626 <223> OTHER INFORMATION:
E--> 1628 <400> SEQUENCE: ①23

1629 Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
E--> 1630 1 5 10

1632 Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
E--> 1633 20 25

1635 Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
E--> 1636 35 40

1638 Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
E--> 1639 50 55

1641 Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
E--> 1642 65 70

1644 Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu
E--> 1645 80 85

1647 Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser
E--> 1648

*misaligned
hos.*

misaligned hos.

	1650 Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala	95	100
E-->	1651		
		110	115
	1653 Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg		
E-->	1654		
		125	130
E-->	1656 Ser Val Gln Leu Tyr Arg <i>invalid</i> Thr Lys Ser Trp Trp Ser Phe Asn		
E-->	1657		
		140	145
	1659 Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser		
E-->	1660		
		155	160
	1662 Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr		
E-->	1663		
		170	175

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1665 Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly
E--> 1666 185 190

1668 Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr
E--> 1669 200 205

1671 Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys
E--> 1672 215 220

1674 Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala
E--> 1675 230 235

1677 Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His
E--> 1678 245 250

1680 Glu Lys Leu Leu His Met Val
1681 260

1684 <210> SEQ ID NO: 24
1686 <211> LENGTH: 377
1688 <212> TYPE: PRT
1690 <213> ORGANISM: feline infectious peritonitis virus
1692 <220> FEATURE:
1694 <223> OTHER INFORMATION:

E--> 1696 <400> SEQUENCE: ①24
1697 Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser
E--> 1698 1 5 10

1701 Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp
E--> 1702 20 25

1705 Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser
E--> 1706 35 40

1709 Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile
E--> 1710 50 55

1713 Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg
E--> 1714 65 70

1717 Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp
E--> 1718 80 85

1721 Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
E--> 1722 95 100

1725 Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala
E--> 1726 110 115

1729 Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu
E--> 1730 125 130

1733 Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln
E--> 1734

*misaligned
ws*

1737 Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln E--> 1738	140	145
1741 Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His E--> 1742	155	160
1745 His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala E--> 1746	170	175
1749 Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser E--> 1750	185	190
1753 Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro E--> 1754	200	205
	215	220

Misaligned LOS.

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
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1757 Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
E--> 1758 230 235 *misaligned nos*

1761 Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe
E--> 1762 245 250

1765 Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr
E--> 1766 260 265

1769 Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe
E--> 1770 275 280

1773 Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val
E--> 1774 290 295

1777 Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr
E--> 1778 305 310

E--> 1781 Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg *involved* Pro Ser Glu
E--> 1782 320 325

1785 Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala
E--> 1786 335 340 345

1789 Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr
E--> 1790 350 355 360

1793 Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
E--> 1794 365 370 375

1797 Thr Asn
1798 377

1800 <210> SEQ ID NO: 25
1802 <211> LENGTH: 642 *please ensure 642 amino acids are present in the sequence*
1804 <212> TYPE: PRT
1806 <213> ORGANISM: feline leukemia virus
1808 <220> FEATURE:
1810 <223> OTHER INFORMATION:

E--> 1812 <400> SEQUENCE: ①25
1813 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
E--> 1814 1 5 10 *misaligned nos*

1816 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
E--> 1817 20 25

1819 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
E--> 1820 35 40

1823 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr
1824 50 55 60
1826 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val
1827 65 70 75
1829 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

del

1830	80	85	90
E--> 1832 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys			
E--> 1833	95	100	105
1835 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr			
E--> 1836	110	115	120
1838 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys			
E--> 1839	125	130	135
1841 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp			
E--> 1842	140	145	150

RAW SEQUENCE LISTING

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```

      1844 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser
E--> 1845                               155                               160                               165
      1847 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser
E--> 1848                               170                               175                               180
      1850 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys
E--> 1851                               185                               190                               195
      1853 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg
E--> 1854                               200                               205                               210
      1856 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser
E--> 1857

      1859 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
E--> 1860                               230                               235                               240
      1862 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr
E--> 1863                               245                               250                               255
      1865 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala
E--> 1866                               260                               265                               270
      1868 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly
E--> 1869                               275                               280                               285
      1871 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala
E--> 1872                               290                               295                               300
      1874 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys
E--> 1875                               305                               310                               315
      1877 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly
E--> 1878                               320                               325                               330
      1880 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile
E--> 1881                               335                               340                               345
      1883 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met
E--> 1884                               350                               355                               360
      1886 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys
E--> 1887                               365                               370                               375
      1889 Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn
E--> 1890                               380                               385                               390
      1892 Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser
E--> 1893                               395                               400                               405
      1895 Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
E--> 1896                               410                               415                               420
      1898 Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
E--> 1899                               425                               430                               435
      1901 His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile Ser Leu
E--> 1902                               440                               445                               450
      1904 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
E--> 1905                               455                               460                               465
      1907 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
E--> 1908                               470                               475                               480
      1910 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
E--> 1911                               485                               490                               495
      1913 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
E--> 1914                               500                               505                               510
      1916 Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu

```

215

220

*misaligned
108*

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```

E--> 1917          515          520          525
      1919 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
E--> 1920          530          535          540
      1922 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
E--> 1923          545          550          555
      1925 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
E--> 1926          560          565          570
      1928 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
E--> 1929          575          580          585
      1931 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Ile
E--> 1932          590          595          600
      1934 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val
E--> 1935 Invalid 605          610          615
E--> 1937 Lys Asp Arg Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln
E--> 1938          620          625          630
      1940 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
E--> 1941          635          640

```

fyf
Please Note:

Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:224 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:1
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0

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L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:310 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:391 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:1
 L:392 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:3
 L:392 M:252 E: No. of Seq. differs, <211>LENGTH:Input:44 Found:40 SEQ:3
 L:406 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:1
 L:418 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:422 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:1
 L:434 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:438 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:1
 L:455 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:1
 L:645 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:649 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:1
 L:670 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:674 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:1
 L:694 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:698 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:1
 L:710 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:714 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:1
 L:726 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:730 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:1
 L:742 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:746 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:1
 L:758 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:762 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:14 differs:1
 L:774 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:778 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:1
 L:790 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:794 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:1
 L:811 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:17 differs:1
 L:851 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:898 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:18 differs:1
 L:984 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1016 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:1
 L:1017 M:254 E: No. of Bases conflict, LENGTH:Input:50 Counted:51 SEQ:19
 L:1017 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 M:254 Repeated in SeqNo=19
 L:1139 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1185 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1190 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1196 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1980 SEQ:19
 L:1211 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:1
 L:1213 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
 M:332 Repeated in SeqNo=20
 L:1268 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

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L:1348 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:1
L:1350 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=21
L:1414 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1479 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:1
L:1481 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=22
L:1628 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:1
L:1630 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=23
L:1656 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1696 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:1
L:1698 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=24
L:1781 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1812 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:1
L:1814 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=25
L:1832 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1901 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1937 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1941 M:252 E: No. of Seq. differs, <211>LENGTH:Input:642 Found:641 SEQ:25